

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101568737
Source: TFW/P
Date Processed by STIC: 2/27/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/568,737

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING DATE: 02/27/2006
 PATENT APPLICATION: US/10/568,737 TIME: 15:06:53

Input Set : A:\PTO.RJ.txt
 Output Set: N:\CRF4\02272006\J568737.raw

3 <110> APPLICANT: SHIRE BIOCHEM INC.
 5 <120> TITLE OF INVENTION: POLYPEPTIDES OF STREPTOCOCCUS PYOGENES
 7 <130> FILE REFERENCE: 51564-44
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/568,737
 C--> 10 <141> CURRENT FILING DATE: 2006-02-15
 12 <150> PRIOR APPLICATION NUMBER: US 60/495,094
 13 <151> PRIOR FILING DATE: 2003-08-15
 15 <160> NUMBER OF SEQ ID NOS: 44
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 537
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Streptococcus pyogenes
 24 <400> SEQUENCE: 1
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 29 attgaaatca aagttaaagg gactgaaatc acagttgtac gtcttaacga ctcaaaaagaa 180
 31 atgaaaacaa tccatgttac aaccctgtct aacttgaata acatggttgt aggtgtttct 240
 33 gaaggtttca aaaaagatct tgaaatgaag ggtgtcggtt accgtgctca acttcaaggt 300
 35 actaaacttg tcctttcagt aggttaatct caccaagacg aagttgaagc tccagaagga 360
 37 attactttca ctgttgcata cccaaacttca atctcagttg aaggaaatcaa caaagaagtt 420
 39 gttggtcaaa cagctgctta catccgttagc ttgcgttac cagagcctta caaaggcaaa 480
 41 gggatccgtt acgttggta atacgtacgc cttaaagaag gtaaaacagg taaataaa 537
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 46 <212> TYPE: PRT
 47 <213> ORGANISM: Streptococcus pyogenes
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 56 20 25 30
 59 Leu Thr Arg Glu Phe Asn Lys Asn Ile Glu Ile Lys Val Glu Gly Thr
 60 35 40 45
 63 Glu Ile Thr Val Val Arg Pro Asn Asp Ser Lys Glu Met Lys Thr Ile
 64 50 55 60
 67 His Gly Thr Thr Arg Ala Asn Leu Asn Asn Met Val Val Gly Val Ser
 68 65 70 75 80
 71 Glu Gly Phe Lys Lys Asp Leu Glu Met Lys Gly Val Gly Tyr Arg Ala
 72 85 90 95
 75 Gln Leu Gln Gly Thr Lys Leu Val Leu Ser Val Gly Lys Ser His Gln
 76 100 105 110
 79 Asp Glu Val Glu Ala Pro Glu Gly Ile Thr Phe Thr Val Ala Asn Pro

Does Not Completely
Corrected Diskette Needed
(Pg. 5)

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Input Set : A:\PTO.RJ.txt
 Output Set: N:\CRF4\02272006\J568737.raw

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84	130	135	140	
87	Ala Ala Tyr Ile Arg Ser Leu Arg Ser Pro Glu Pro Tyr Lys Gly Lys			
88	145	150	155	160
91	Gly Ile Arg Tyr Val Gly Glu Tyr Val Arg Leu Lys Glu Gly Lys Thr			
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95	Gly Lys			
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100	<211> LENGTH: 1269			
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102	<213> ORGANISM: Streptococcus pyogenes			
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109	tcttagtgtca acaaaggtaaa agcctaacc ataaaagaag ccatggaca aggaaaagat		180	
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113	tcaagtaaaag gagaagtcaa agaggtcttt gttaaaaaaag gcgatgttgc caaagttagga		300	
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125	gctactgcacca aacggaaaaa aggttaacta gatgtgaca ccgttaagtc agacaccgca		660	
127	ggaaccatgt ttagtctaaa tactgatttg ccaaataatc caaaatccaa aaaagaaaaat		720	
129	gaaactttta tggaaattat cgacaaatca aaaatgttag tcaaaggtaa cattagtgaa		780	
131	tttgaccctgtg acaagttaaa aatcggtcaa aaagtgcgaag tgattgaccg caaagacaac		840	
133	tctaaaaat ggactggaaa agtaacccca gttggcaacc tcaaaggcaga ggaaaaaggc		900	
135	caaggtcaag gccaaaggtaaa caatgaccaaa caagataatc caaaaccaagc aaaattccct		960	
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162	20	25	30	
165	Asn His Gln Gln Gln Glu Ile Val Ser Ser Val Asn Lys Val Lys Ala			
166	35	40	45	
169	Leu Thr Ile Lys Glu Ala Met Glu Gln Gly Lys Asp Ile Ser Leu Thr			
170	50	55	60	
173	Leu Ala Gly Glu Val Thr Ala Asn Asn Ser Ser Lys Val Lys Ile Asp			

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174	65	70	75	80
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181	Val Lys Val Gly Gln Pro Leu Phe Ser Tyr Glu Thr Ser Gln Arg Leu			
182	100	105	110	
185	Thr Ala Gln Ser Ser Glu Phe Asp Val Gln Thr Lys Ala Asn Gln Leu			
186	115	120	125	
189	Gln Val Ala Lys Thr Asn Ala Ala Leu Lys Trp Glu Thr Tyr Asn Arg			
190	130	135	140	
193	Lys Val Asn Glu Ile Asn Thr Leu Lys Ser Arg Tyr Asn Thr Ala Pro			
194	145	150	155	160
197	Asp Glu Ser Leu Leu Glu Gln Ile Arg Ser Ala Glu Asp Ser Val Ser			
198	165	170	175	
201	Gln Ala Leu Ser Asp Ala Lys Thr Ala Asp Ser Asp Val Lys Thr Ala			
202	180	185	190	
205	Gln Ile Glu Leu Asp Lys Ala Asn Ala Thr Ala Thr Thr Glu Lys Gly			
206	195	200	205	
209	Lys Leu Glu Tyr Asp Thr Val Lys Ser Asp Thr Ala Gly Thr Ile Val			
210	210	215	220	
213	Ser Leu Asn Thr Asp Leu Pro Asn Gln Ser Lys Ser Lys Lys Glu Asn			
214	225	230	235	240
217	Glu Thr Phe Met Glu Ile Ile Asp Lys Ser Lys Met Leu Val Lys Gly			
218	245	250	255	
221	Asn Ile Ser Glu Phe Asp Arg Asp Lys Leu Lys Ile Gly Gln Lys Val			
222	260	265	270	
225	Glu Val Ile Asp Arg Lys Asp Asn Ser Lys Lys Trp Thr Gly Lys Val			
226	275	280	285	
229	Thr Gln Val Gly Asn Leu Lys Ala Glu Glu Lys Gly Gln Gly Gln Gly			
230	290	295	300	
233	Gln Gly Gly Asn Asp Gln Gln Asp Asn Pro Asn Gln Ala Lys Phe Pro			
234	305	310	315	320
237	Tyr Val Ile Glu Leu Asp Gln Ser Asp Lys Gln Pro Leu Ile Gly Ser			
238	325	330	335	
241	His Thr Tyr Val Asn Val Leu Asn Asn Val Pro Glu Ala Gly Lys Ile			
242	340	345	350	
245	Val Leu Lys Glu Thr Phe Thr Met Ala Glu Asn Gly Lys Thr Tyr Val			
246	355	360	365	
249	Trp Lys Val Asp Lys Asn Lys Val Lys Lys Gln Glu Ile Lys Thr Lys			
250	370	375	380	
253	Pro Phe Ser Lys Gly Tyr Val Glu Val Thr Ser Gly Leu Thr Met Gln			
254	385	390	395	400
257	Asp Lys Ile Ala Gln Pro Leu Pro Gly Met Lys Asp Gly Met Glu Val			
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261	Gly Ser Ile Val Lys Pro			
262	420			
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266	<211> LENGTH: 885			
267	<212> TYPE: DNA			
268	<213> ORGANISM: Streptococcus pyogenes			

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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272006\J568737.raw

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 271 atgataaaac gatgtaaaagg aattgggtcta gccttaatgg ccttctttt gtagcttg 60
 273 gtgaatcagc accctaaaac ggctaaagag actgaacagc agagaattgt agccacttcg 120
 275 gttgctgtgg ttgatatctg tgaccgtta aatttagacc tcgttgggtt ttgtgatagt 180
 277 aaatttatata cccttcctaa acgctatgat gctgttaagc gtgtgggtt acccatgaat 240
 279 cctgatatacg agttgattgc ttcttgaaa ccaacttggg ttttgagtcc caattctta 300
 281 caagaagatt tggAACCCAA gtataaaaaa ttggatactg agtatgggtt ttgaaactta 360
 283 cgaagtgttggggcatgtc ccagtcattt gatgatttt ggaacctttt ccaacgtcaa 420
 285 caagaagcaa aagaattgcg ccagcaatac caggactatt atcgtctt ccaagctaaa 480
 287 cgtaagggga agaaaaagcc taaagtgtt attcttatgg gcttgcagg tagttatgg 540
 289 gtggcagca accaatctt ttagggat ctttggact tggcaggtgg tgagaatgtt 600
 291 tattcgtcag atgagaaaatgatttctatca gtaatctt aagacatgtt gctaaaggag 660
 293 cctgacttga ttttacgaac agctcatgcc attccagaca agttaaaagt gatgtttgac 720
 295 aaagaatttg ctgaaaaatga tattggaaa cattttacgg cagtcaagga agggaaagtc 780
 297 tatgatttgg acaataccct gtttgcattt gatgtctt aat tgaactaccc agaagccttg 840
 299 gacaccttaa cacagcttt tgaccacgtg ggagatcattt cgtaa 885
 302 <210> SEQ ID NO: 6
 303 <211> LENGTH: 294
 304 <212> TYPE: PRT
 305 <213> ORGANISM: Streptococcus pyogenes
 307 <400> SEQUENCE: 6
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 313 Leu Val Ala Cys Val Asn Gln His Pro Lys Thr Ala Lys Glu Thr Glu
 314 20 25 30
 317 Gln Gln Arg Ile Val Ala Thr Ser Val Ala Val Val Asp Ile Cys Asp
 318 35 40 45
 321 Arg Leu Asn Leu Asp Leu Val Gly Val Cys Asp Ser Lys Leu Tyr Thr
 322 50 55 60
 325 Leu Pro Lys Arg Tyr Asp Ala Val Lys Arg Val Gly Leu Pro Met Asn
 326 65 70 75 80
 329 Pro Asp Ile Glu Leu Ile Ala Ser Leu Lys Pro Thr Trp Ile Leu Ser
 330 85 90 95
 333 Pro Asn Ser Leu Gln Glu Asp Leu Glu Pro Lys Tyr Gln Lys Leu Asp
 334 100 105 110
 337 Thr Glu Tyr Gly Phe Leu Asn Leu Arg Ser Val Glu Gly Met Tyr Gln
 338 115 120 125
 341 Ser Ile Asp Asp Leu Gly Asn Leu Phe Gln Arg Gln Gln Glu Ala Lys
 342 130 135 140
 345 Glu Leu Arg Gln Gln Tyr Gln Asp Tyr Tyr Arg Ala Phe Gln Ala Lys
 346 145 150 155 160
 349 Arg Lys Gly Lys Lys Pro Lys Val Leu Ile Leu Met Gly Leu Pro
 350 165 170 175
 353 Gly Ser Tyr Leu Val Ala Thr Asn Gln Ser Tyr Val Glu Asn Leu Leu
 354 180 185 190
 357 Asp Leu Ala Gly Gly Glu Asn Val Tyr Gln Ser Asp Glu Lys Glu Phe
 358 195 200 205
 361 Leu Ser Ala Asn Pro Glu Asp Met Leu Ala Lys Glu Pro Asp Leu Ile
 362 210 215 220

RAW SEQUENCE LISTING
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DATE: 02/27/2006
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Input Set : A:\PTO.RJ.txt
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366 225 230 235 240
369 Lys Glu Phe Ala Glu Asn Asp Ile Trp Lys His Phe Thr Ala Val Lys
370 245 250 255
373 Glu Gly Lys Val Tyr Asp Leu Asp Asn Thr Leu Phe Gly Met Ser Ala
374 260 265 270
377 Lys Leu Asn Tyr Pro Glu Ala Leu Asp Thr Leu Thr Gln Leu Phe Asp
378 275 280 285
381 His Val Gly Asp His Pro
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386 <211> LENGTH: 34
387 <212> TYPE: DNA
388 <213> ORGANISM: Primer
389 <400> SEQUENCE: 7
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413 <211> LENGTH: 38
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422 <211> LENGTH: 35
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424 <213> ORGANISM: Primer
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431 <211> LENGTH: 35
432 <212> TYPE: DNA
433 <213> ORGANISM: Primer
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439 <210> SEQ ID NO: 13
440 <211> LENGTH: 30
441 <212> TYPE: DNA

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The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sections for similar errors.

INVALID RESPONSE

INVALID RESPONSE

Same error

Same error

Same error

Same error

Same error

See item

10 on

error

Summary

Sheet

VERIFICATION SUMMARY **DATE:** 02/27/2006
PATENT APPLICATION: US/10/568,737 **TIME:** 15:06:54

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272006\J568737.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application
Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date